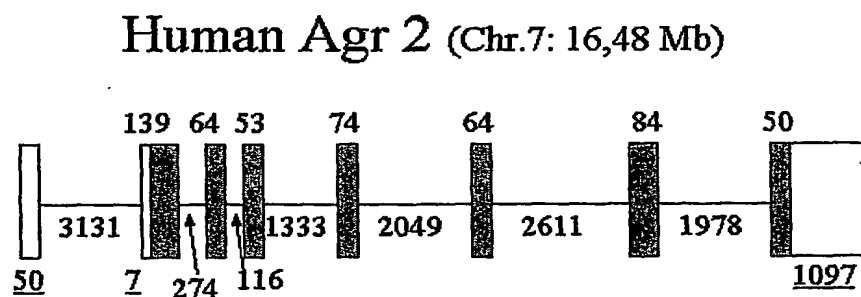
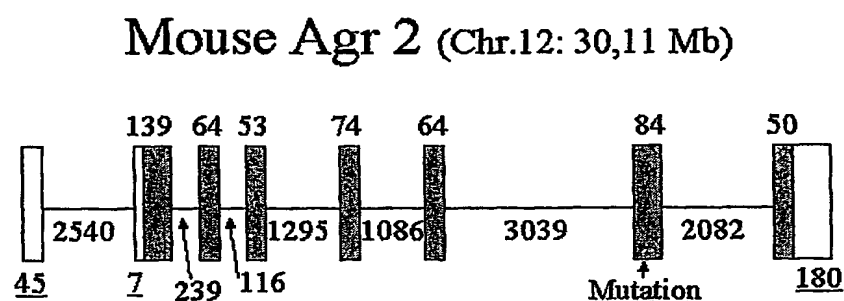


Figure 1A.

Mouse	Gene ID	Mouse Gene Description	Chr	Map Start	Human	Gene ID	Human Gene Description	Chr	Map Start
	092324	NEPHRIN OF ATONAL 3	12	28041829		096R36	NEPHRIN OF ATONAL 3	7	18829031
NH 011658		TWIST RELATED PROTEIN (H-TWIST)	12	28071270			TWIST RELATED PROTEIN (H-TWIST)	7	18800882
NH 024124		HISTONE DEACETYLASE 9 (HD9) (HD7B)	12	28488280	NH 014707		HISTONE DEACETYLASE 9 (HD9) (HD7B) (HD7)	7	18179912
NH 013464		AH RECEPTOR PRECURSOR (AHR)	12	29623298			AH RECEPTOR (ARYL HYDROCARBON RECEPTOR) (AHR)	7	16982797
BC023499		SIMILAR TO ANTERIOR GRADIENT PROTEIN 3	12	30054071		08YD06	ANTERIOR GRADIENT PROTEIN 3	7	16543709
046912		ANTERIOR GRADIENT 2 HOMOLOG (XENopus LARVIS)	12	30112593	BC023499		ANTERIOR GRADIENT 2 HOMOLOG (XENopus LARVIS)	7	16460023
HOM2 MOUSE		HOMEOBOX PROTEIN HOX-2	12	31233665	HOM2		HOMEOBOX PROTEIN HOX-2	7	15295209
NH 007960		ETS1 PROTEIN (ETS TRANSLOCATION VARIANT 1)	12	32910756		ETV1	ETS TRANSLOCATION VARIANT 1 (ETS1 PROTEIN)	7	13579610
NH 007487		ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 4	12	34165437		ARL4	ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 4	7	12370905
NH 009132		ADSERVIN (SCINDERIN) (GELSOLIN-LIKE PROTEIN)	12	34189389		096PT2	ADSERVIN (SCINDERIN)	7	12254575

Figure 1B.



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Figure 2.

BLAST 2 Sequences

(<http://www.ncbi.nlm.nih.gov/blast/bl2seq/bl2.html>)

Sequence 1: mouse AGR2 (WT); SEQ ID No:3

Sequence 2: human AGR2 (WT); SEQ ID No:4

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database.

Score = 323 bits (828), Expect = 4e-88

Identities = 160/175 (91%), Positives = 168/175 (95%)

```

Query: 1  MEKFSVSAILLLVAISGTLAKDTTVKSGAKKDPKDSRPKLPQTLSRGWGDQLIWTQTYEE 60
          MEK  VSA LLLVA+S TLA+DTTVK GAKKD KDSRPKLPQTLSRGWGDQLIWTQTYEE
Sbjct: 1  MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE 60

Query: 61  ALYRSKTSNRPLMVIHHLDECPHSQALKKVFAEHKEIQKLAEQFVLLNLVYETTDKHLSP 120
          ALY+SKTSN+PLM+IHHLDECPHSQALKKVFAE+KEIQKLAEQFVLLNLVYETTDKHLSP
Sbjct: 61  ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP 120

Query: 121 DGQYVPRIVFVDPSLTIVRADITGRYSNRLYAYEPSDTALLYDNMKKALKLLKTEL 175
          DGQYVPRI+FVDPSLTIVRADITGRYSNRLYAYEP+DTALL DNMKKALKLLKTEL
Sbjct: 121 DGQYVPRIMFVDPSLTIVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL 175

```

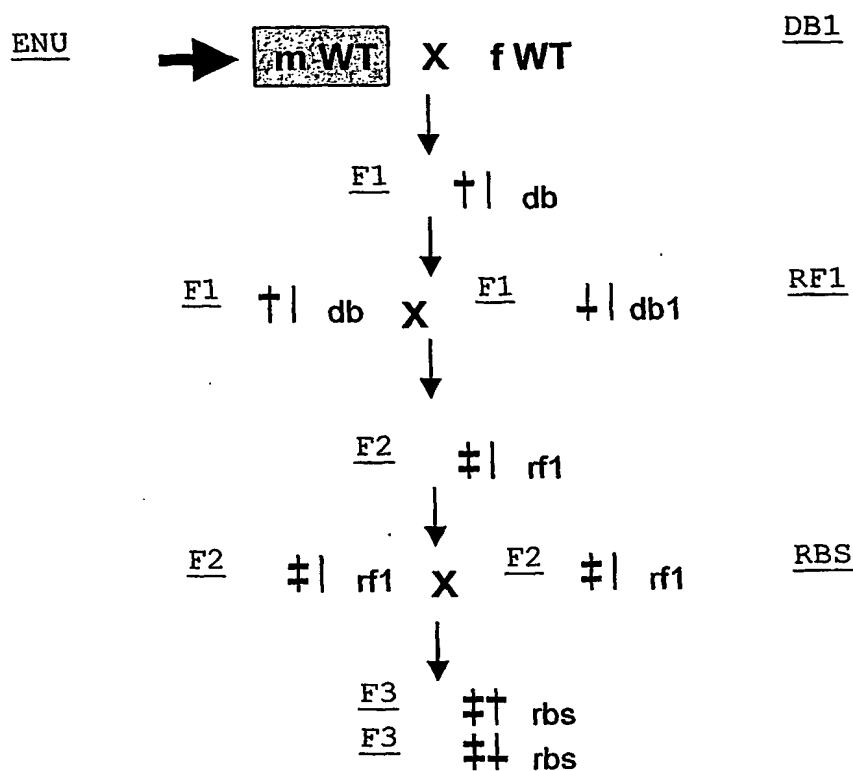
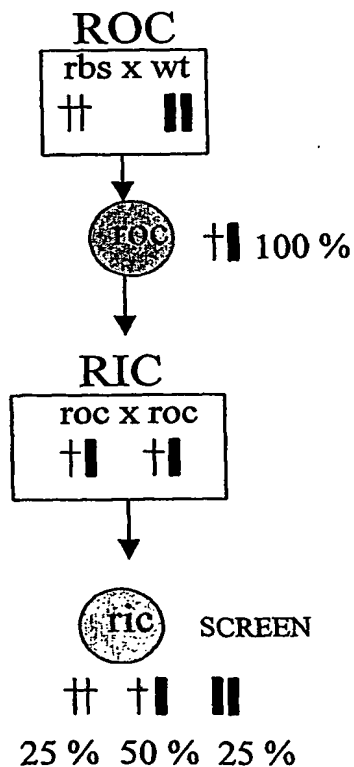
Figure 3.**Breeding-Scheme:**
A) F3 production**B) Outcross**

Figure 4.

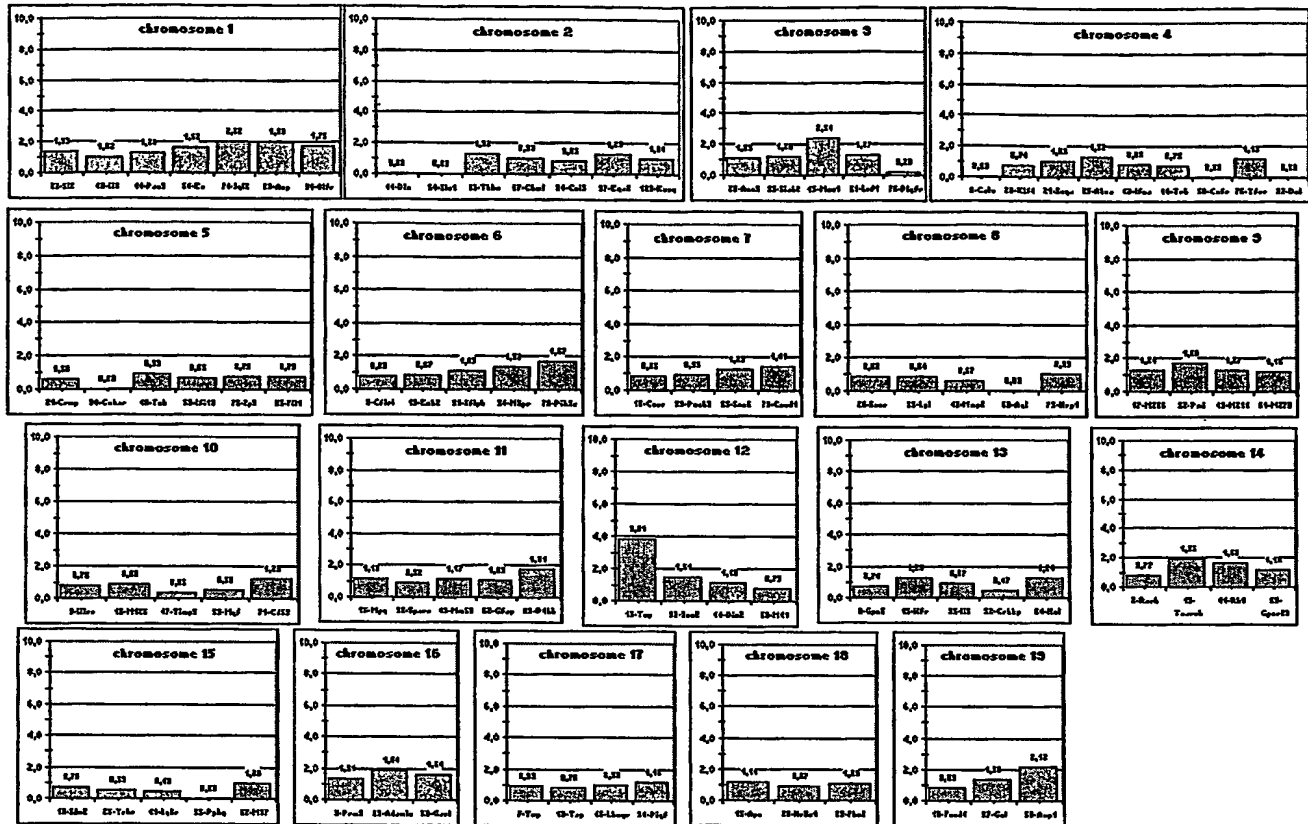


Figure 5.**Haplotypes Scheme**

























appr. cM	Marker	appr. Mb			
6	D12Mit12	18,7			
7	Idb2	19,1			
<hr/>					
10	D12Mit171	23,4			
8	Slc26a3	25,5			
14	D12Mit221	40,3			
<hr/>					
18	D12Mit64	44,8			
19	D12Mit110	46,3			
25	D12Mit285	49,1			
			SEX	m	f
			MOUSE	#899	#99
					m
					#64

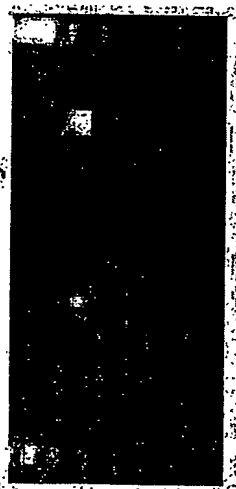
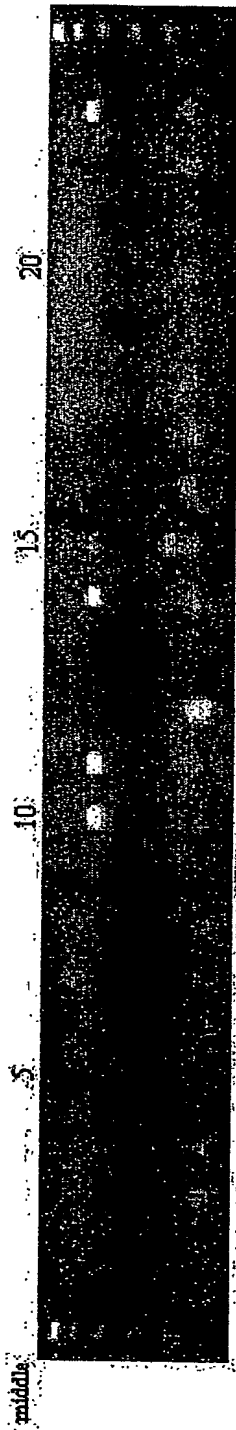
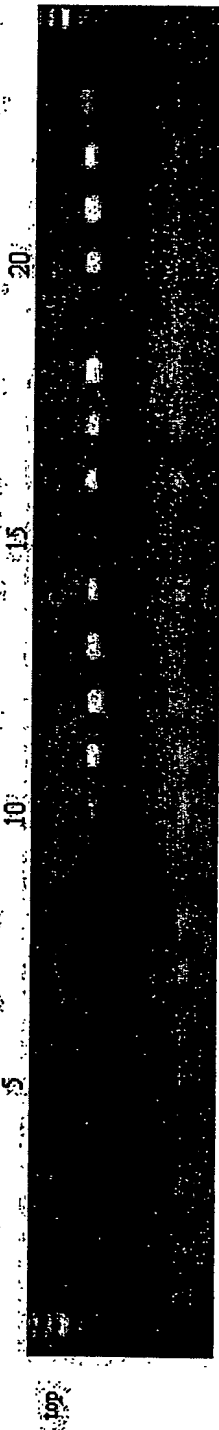
Figure 6

primer: Mm Arg2-7/2 (349 bp)

project: mAg2

gender specific female organs + embryo

Tissue cDNA panel C3H male



top:
Marker 100 bp ladder
1 total brain
2 olfactory lobes
3 cerebrum
4 cerebrum left hemisphere
5 cerebrum right hemisphere
6 cerebellum
7 pituitary gland
8 mesencephalon
9 mesencephalon
10 eye
11 nose
12 trachea
13 thyroid gland
14 lung
15 tongue
16 esophagus
17 salivary gland
18 stomach
19 pancreas
20 small intestine
21 large intestine
22 appendix
23 rectum
24 thymus
Marker 100 bp ladder

middle:
Marker 100 bp ladder
1 lymph nodes
2 heart
3 mesenterium
4 gall bladder
5 liver
6 spleen
7 kidney
8 adrenal gland
9 bladder
10 testis
11 epididymis
12 prostate
Marker 100 bp ladder

bottom:
Marker 100 bp ladder
1 Embryo d 13.5 head
2 Embryo d 13.5 body
3 Embryo d 18.5 head
4 Embryo d 18.5 body
5 Embryo d 10-12 (Arabidopsis)
6 pool
7 neg. control
Marker 100 bp ladder
13 ovary
14 uterus
15 placenta
16 sternum
17 bone marrow
18 whole blood
19 skin
20 adipose tissue
21 skeletal muscle
22 ES cells
23 Embryo d 5.5
24 Embryo d 9.5
Marker 100 bp ladder

Figure 7.

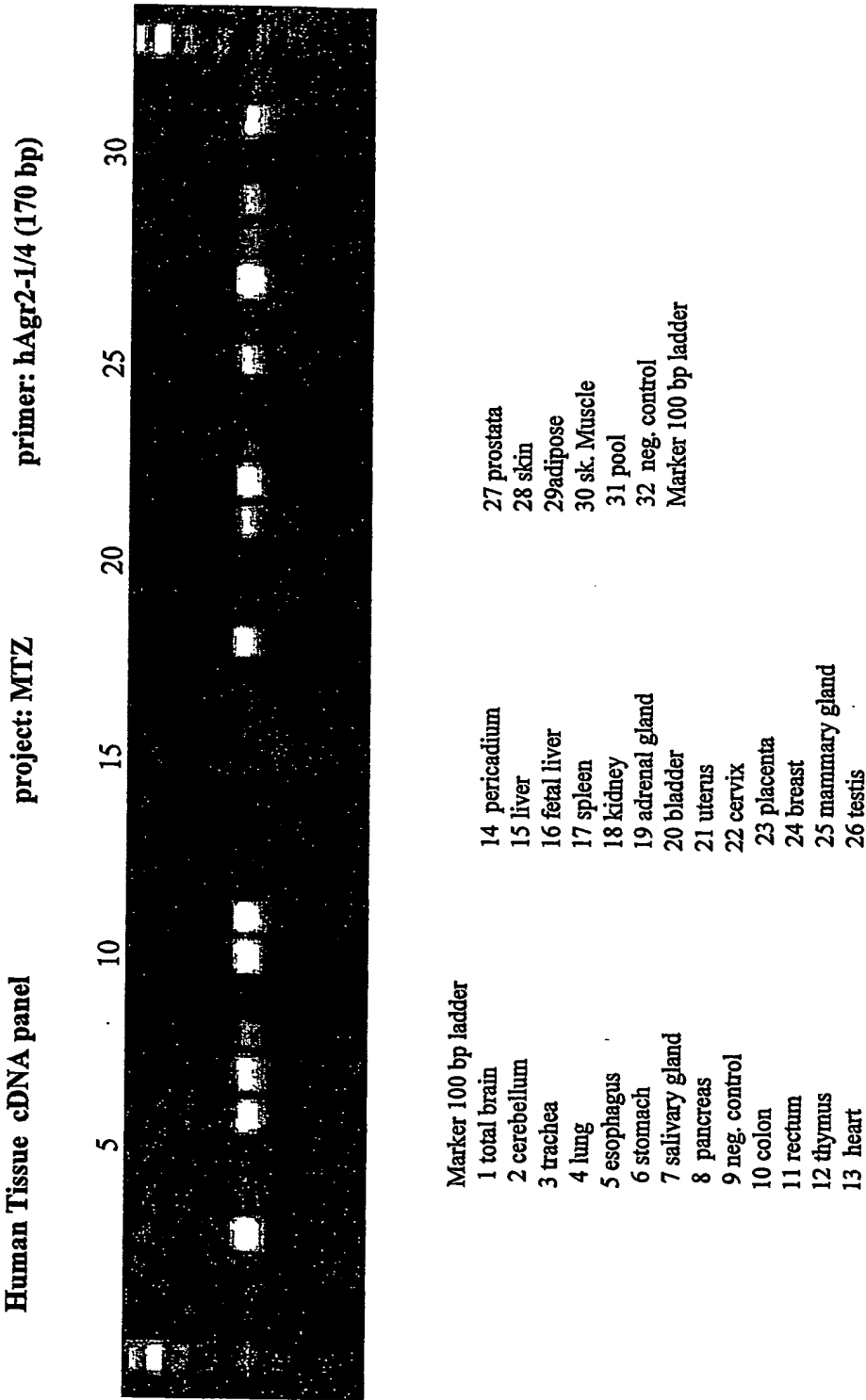


Figure 8.

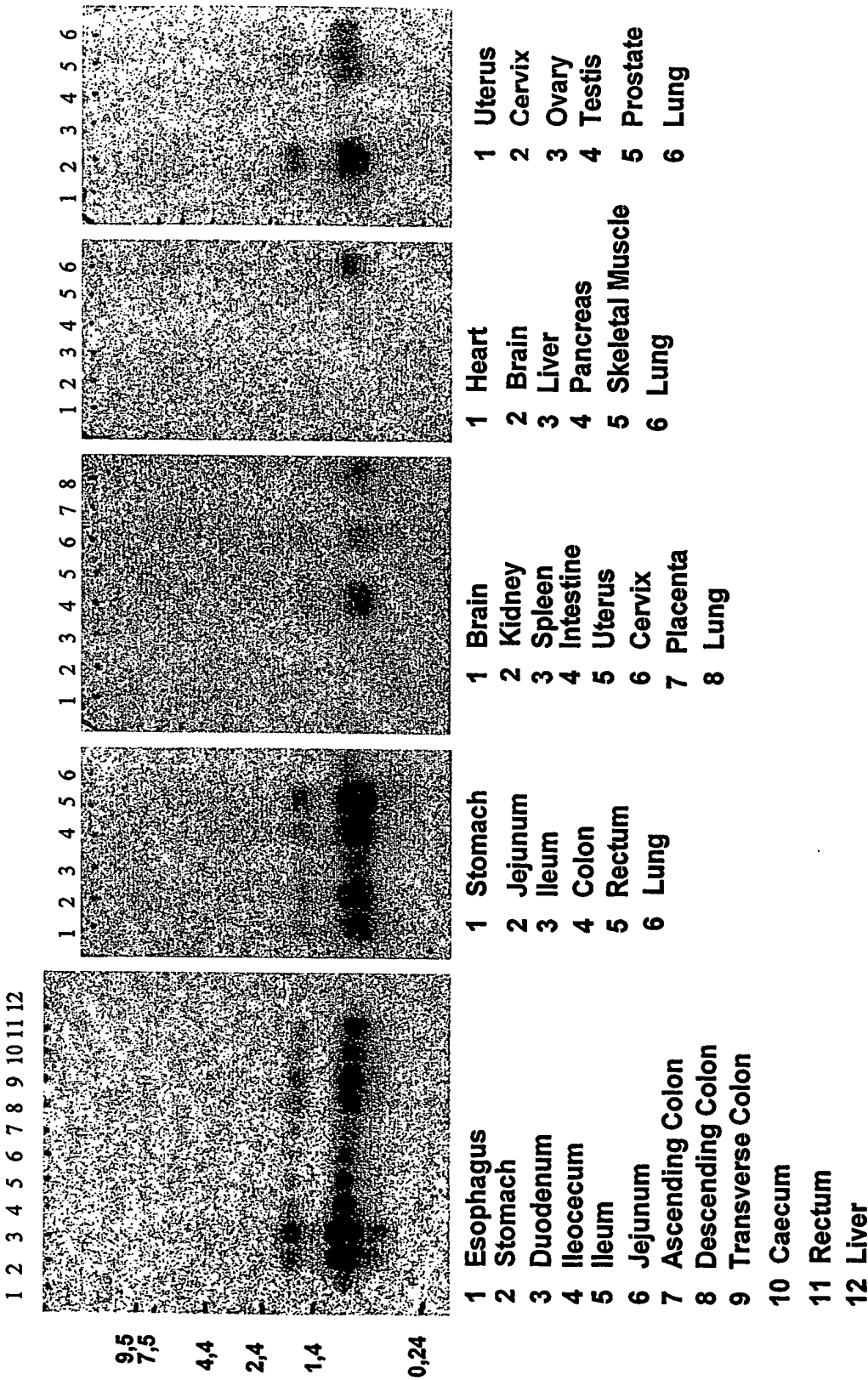


Figure 9.

mouse number	agr2 genotype	thriving deficit	chronic diarrhea
1	mut	yes	yes
2	mut	yes	yes
3	mut	yes	yes
4	mut	yes	yes
5	mut	yes	yes
6	hz	no	no
7	hz	no	no
8	hz	no	no
9	hz	no	no
10	hz	no	no
11	hz	no	no
12	hz	no	no
13	hz	no	no
14	hz	no	no
15	hz	no	no
16	hz	no	no
17	hz	no	no
18	hz	no	no
19	wt	no	no
20	wt	no	no
21	wt	no	no
22	wt	no	no
23	wt	no	no
24	wt	no	no
25	wt	no	no

Figure 10.

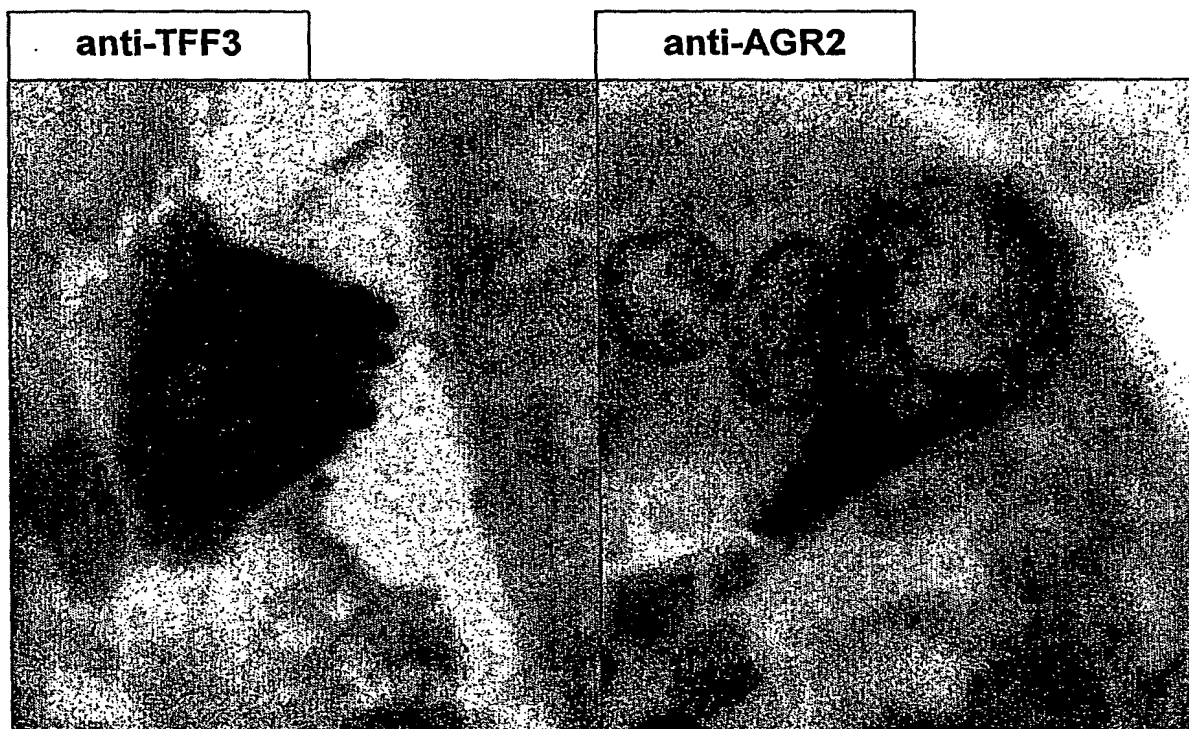


Figure 11.

Colon (wild type mouse)



Colon (affected mouse)



Figure 12.

Colon (affected mouse)

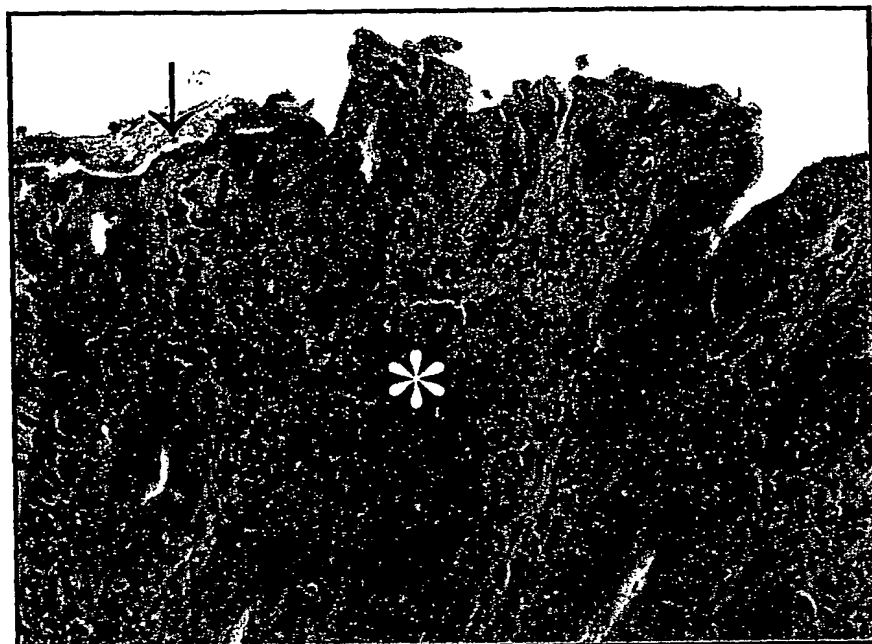
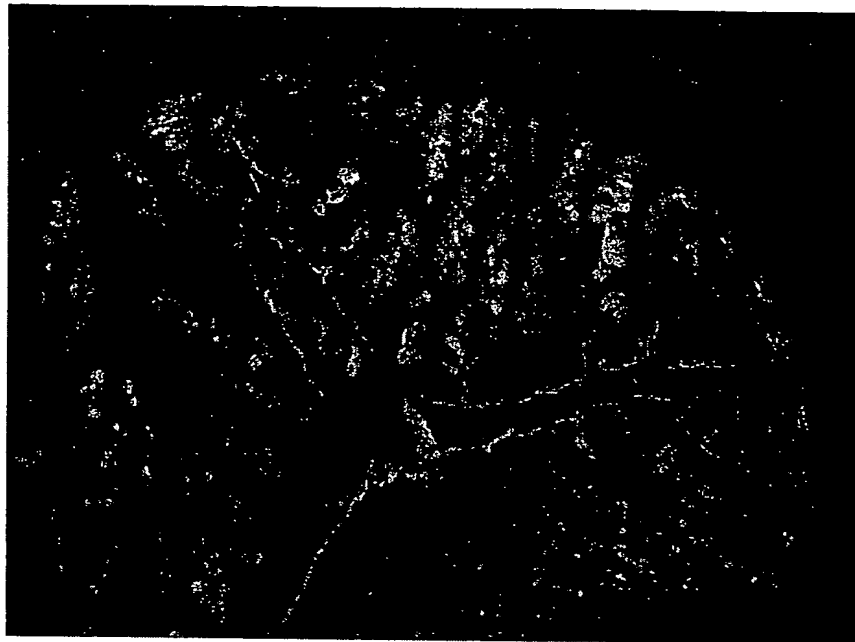


Figure 13.

Colon (wild type mouse)

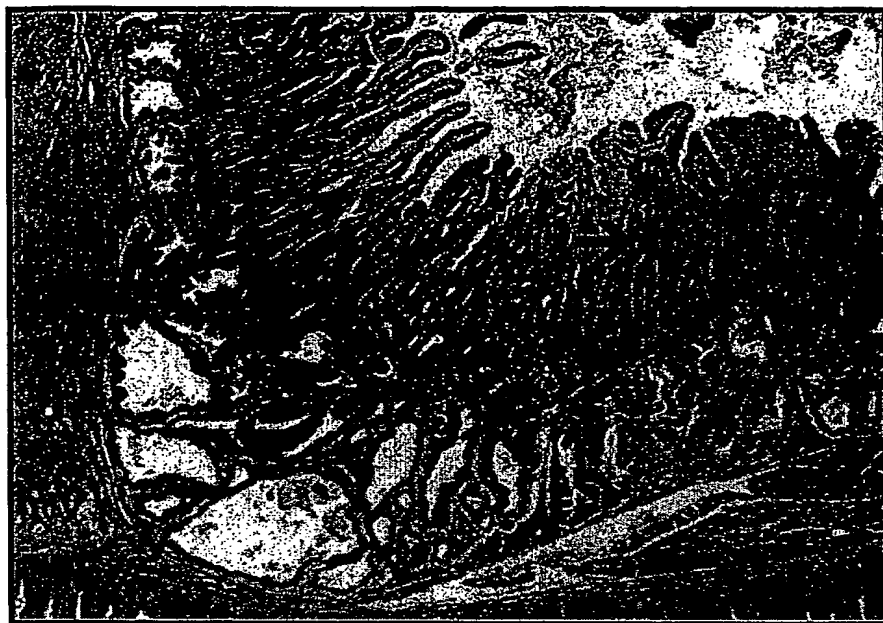


Colon (affected mouse)



Figure 14.

Brunner's gland (wild type mouse)



Brunner's gland (affected mouse)



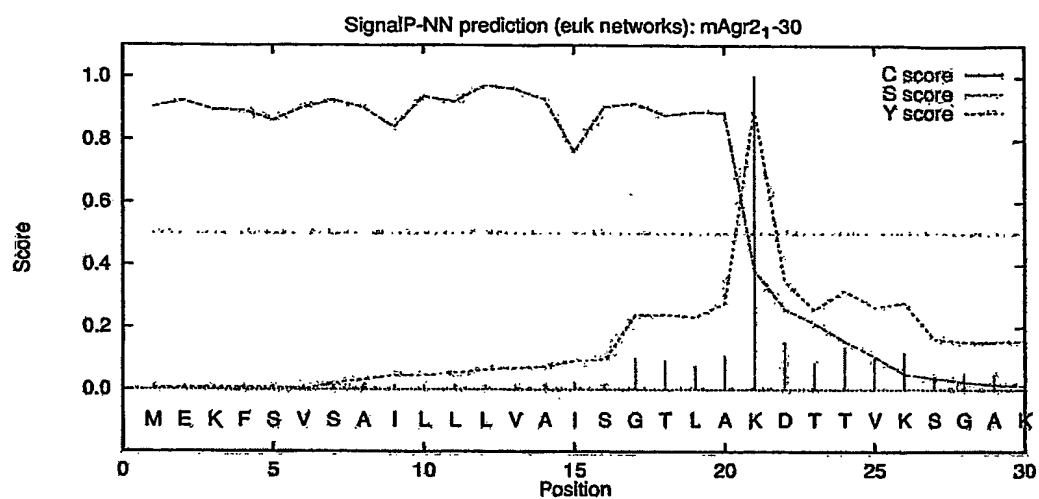
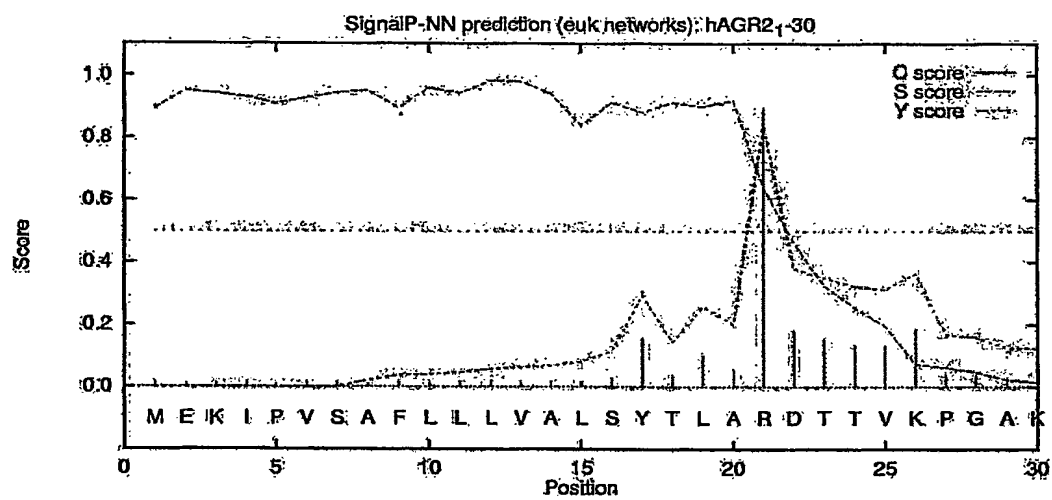
Figure 15A.**Figure 15B.**

Figure 16.

Software used:

- MultAlin via <http://prodes.toulouse.inra.fr/multalin/multalin.html> [Corpet. F. (1988), Multiple sequence alignment with hierarchical clustering, Nucl. Acids Res., 16 (22), 10881-10890]
- BOXSHADE 3.21 via http://www.ch.embnet.org/software/BOX_form.html

Mm: Mus musculus; NP_035913

Hs: Homo sapiens; NP_006399

Rn: Rattus norvegicus; derived by Genewise on AC126809

Mm	1	MEKFSVSAILLLVAISGTLAKDTTVKSGAKKDPKDSRPKLPQTLSRGWDQLIWTQTYEE
Rn	1	MEKFSVSAILLLVAISGTLAKDTTVKSGAKKDPKDSRPKLPQTLSRGWDQLIWTQTYEE
Hs	1	MEKIPVSAIFLLLVAFSYTLAKDTTVKPGAKKDTKDSRPKLPQTLSRGWDQLIWTQTYEE
Consensus	1	MEKFSVSAILLLVAISGTLAKDTTVKSGAKKDPKDSRPKLPQTLSRGWDQLIWTQTYEE

Mm	61	ALYKSKTSNRPLMVIHHLDECPHSQALKKVFAEHKEIQKLAEQFVLLNLVYETTDKHLSP
Rn	61	ALYKSKTSNRPLMVIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
Hs	61	ALYKSKTSNKPMLTIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
Consensus	61	ALYKSKTSNRPLM!IHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNL!YETTDKHLSP

▼MTZ (VVE)

Mm	121	DGQYVPRIVFVDPSLTVRADITGRYSNRLYAYEPSDTALLYDNMKKALKLLKTEL
Rn	121	DGQYVPRIVFVDPSLTVRADITGRYSNRLYAYEPSDTALLHDNMKKALKLLKTEL
Hs	121	DGQYVPRIFVVDPSLTVRADITGRYSNRLYAYEPADTALLDNMKKALKLLKTEL
Consensus	119	DGQYVPRIVFVDPSLTVRADITGRYSNRLYAYEPSDTALL.DNMKKALKLLKTEL

Percentage of identical and similar amino acids:	95.4%
Percentage of identical amino acids:	90.8%

Figure 17.

Software used:

- MultAlin via <http://prodes.toulouse.inra.fr/multalin/multalin.html> [Corpet. F. (1988), Multiple sequence alignment with hierarchical clustering, Nucl. Acids Res., 16 (22), 10881-10890]
- BOXSHADE 3.21 via http://www.ch.embnet.org/software/BOX_form.html

Mm: Mus musculus; NP_035913
 Hs: Homo sapiens; NP_006399
 Rn: Rattus norvegicus; derived by Genewise on AC126809
 Xl: Xenopus laevis; AAL26844

Mm	1	MEKFSVSAIILLVATSGTLAKDTTVKS	SAKKDP	KDSRPKLPQTL	SRGWGDQLIWTQTYEE
Rn	1	MEKFSVSAIILLVATSGTLAKDTTVRS	SAKKDP	KDSRPKLPQTL	SRGWGDQLIWTQTYEE
Hs	1	MEKIPVSAFLLLVATSYTLAKDTTVKN	SAKKDT	KDSRPKLPQTL	SRGWGDQLIWTQTYEE
Xl	1	METVLKSLFILLVATSETLAK	KKPQTL	SRGWGDQLIWTQTYEE
Consensus	1	MEK..VSAFLLVA.S.TLAK#TTVK.	SAKKD.	KDSRPKLPQTL	SRGWGD#LIWTQTYEE

Mm	61	ALYKSKTSNRPPLMIHHLDEC	PHSQALKKVFAEH	KEIQKLAEQFVLLNLVYETTDKHLSP
Rn	61	ALYKSKTSNRPPLMIHHLDEC	PHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP	
Hs	61	ALYKSKTSNKPLMIHHLDEC	PHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP	
Xl	45	GLEKAKSENKPLLLINRHH	CPHSQALKKAF	AEHOGIQKLAEFFLLNLVYETTDKHLSP
Consensus	53	ALYKSKTSNKPLS.IHHL##	CPHSQALKKVFAENKEIQKLAE#F!	LLNL!Y#TTDKHLSP

▼MTZ (VVE)

Mm	121	DGOYVPRIVFVDPSLTVRADITGRYSNRLYAYEP	SDTALLYDNM	KKALKLLKTEL
Rn	121	DGOYVPRIVFVDPSLTVRADITGRYSNRLYAYEP	SDTALLHONM	KKALKLLKTEL
Hs	121	DGOYVPRIVFVDPSLTVRADITGRYSNRLYAYEP	ADTALLLDNM	KKALKLLKTEL
Xl	105	DGOYVPRIVFVDPSLTVRADITGRYSNRLYAYEP	ADIDHLEFNM	KKALVLLKTEL
Consensus	104	DGOYVPRIVFVDPSLTVRADITGRYSNRLYAYEP	ADTALL.#NM	KKALKLLKTEL

Percentage of identical and similar amino acids: 82%
 Percentage of identical amino acids: 67%

Figure 18.**Software used:**

- MultAlin via <http://prodes.toulouse.inra.fr/multalin/multalin.html> [Corpet. F. (1988), Multiple sequence alignment with hierarchical clustering, Nucl. Acids Res., 16 (22), 10881-10890]
- BOXSHADE 3.21 via http://www.ch.embnet.org/software/BOX_form.html

Mm: *Mus musculus*; NP_035913
 Hs: *Homo sapiens*; NP_006399
 Rn: *Rattus norvegicus*; derived by Genewise on AC126809
 Xl: *Xenopus laevis*; AAL26844
 Ce: *Caenorhabditis elegans*; NP_496599

```

Mm      1 MEKFSVSATLLLVATISGTLAKDTTVKSGAKKDKDSRPKLPQTL SRGWGDQLIWTQTYEE
Rn      1 MEKFSVSATLLLVATISGTLAKDTTVKSGSKKDKDSRPKLPQTL SRGWGDQLIWTQTYEE
Hs      1 MEKIPVSATLLLVATISYTLAKDTTVKPKAKKDKDSRPKLPQTL SRGWGDQLIWTQTYEE
Xl      1 METVLKSLFFLLVATSFETLAKD.....KKPQTL SRGWGDQLIWTQTYEE
Ce      1 ....MRSLHLLALVSAAYASFDKIKD.....STONELARGEGLDIAWVK.WED
Consensus 1 MEK..VSA.LLLVA.S.TLAKDTTVK..G.KKD.KDSRPKLE#TL SRGWGD#LIWTQTYE#

```

```

Mm      61 ALYRSKTSNRPIMVIHHLDECPHSQALKKVFAEH...KEIQKLAEQFVLLNLVY..ETTD
Rn      61 ALYRSKTSNRPIMVIHHLDECPHSQALKKVFAEN...KEIQKLAEQFVLLNLVY..ETTD
Hs      61 ALYRSKTSNRPIMVIHHLDECPHSQALKKVFAEN...KEIQKLAEQFVLLNLVY..ETTD
Xl      45 GLEKPKSENKPIILLINHRNICPHSQALKKFAEH...OGIQKLAEQFVLLNLVY..ETTD
Ce      45 ALETALDITKPIELLINKSWCHACKALKKTEQASNAKPAFKKLSHFVHNTEDDDPEFE
Consensus 50 ALYRSKTS#KPLM.IHHLDECPHSQALKKVFA#....KEIQKLAEQF!$NLVY..#TT#

```

▼MTZ (VVE)

```

Mm      116 KHLSPDGQYVPRIVFVDPSLTVRADITGRYSN.RLYAYEPSDTALLYDNMKKALKLLKTE
Rn      116 KHLSPDGQYVPRIVFVDPSLTVRADITGRYSN.RLYAYEPSDTALLHNDNMKKALKLLKTE
Hs      116 KHLSPDGQYVPRIVFVDPSLTVRADITGRYSN.RLYAYEPSDTALLHNDNMKKALKLLKTE
Xl      100 KNLQLDGQYVPRIVFVDPSLTVRADITGRYSN.HQYTEPADIDHLENDNMKKALVLLKTE
Ce      105 EEYRPDGKYLPRLLIFIDKNGDILQEFKNKAEYKNYAYYYSPADILNSMKDVLKHFQVD
Consensus 97 KHLSPDGQY!PRIVFVDPSLTVRA#ITGRYS#.RLYAYEPSDTALL.#NMKKALKLLKT#

```

```

Mm      175 L.....
Rn      175 L.....
Hs      175 L.....
Xl      159 L.....
Ce      165 LPEAKRGDKLKPKKPEGKKKEL
Consensus 150 L.....

```

Percentage of identical and similar amino acids: 32%
 Percentage of identical amino acids: 46%

Figure 19.

mRNA regulation
[fold change relative to
reference marker ALAS]

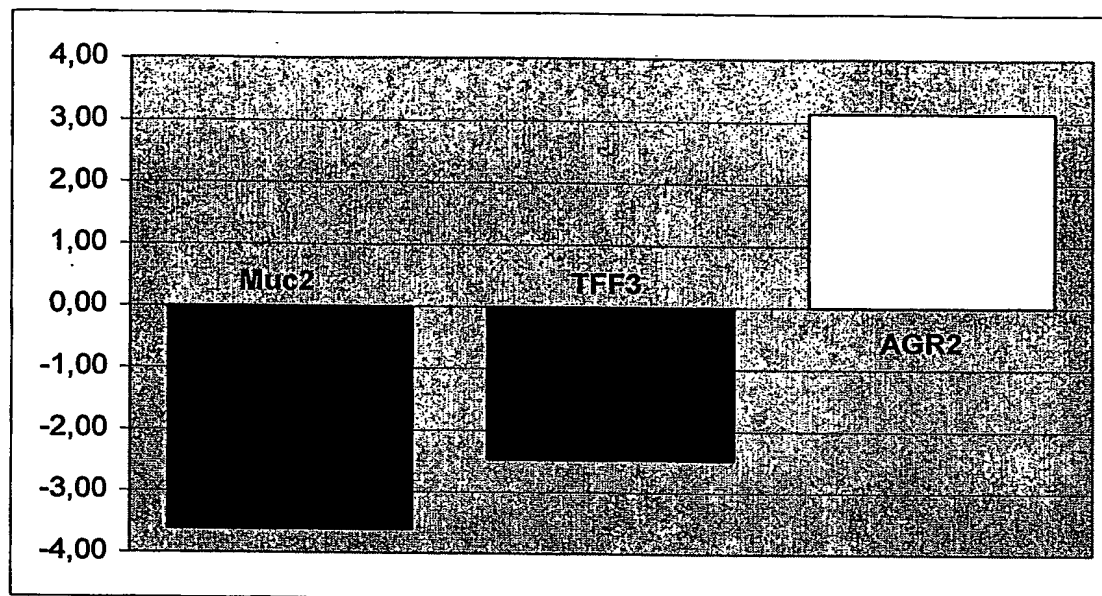
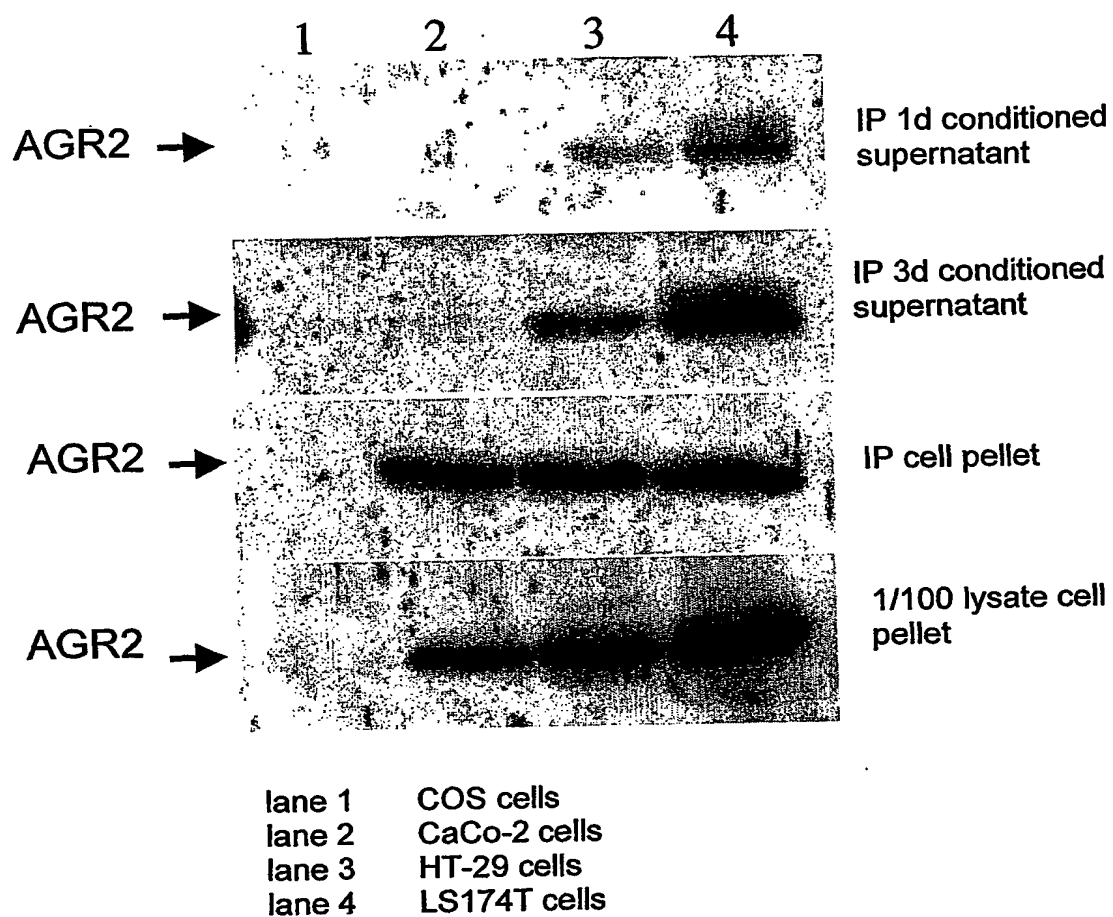


Figure 20.

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